

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/869,565

DATE: 11/14/2001
TIME: 13:57:56

Input Set : A:\sequence listing ascii
Output Set: N:\CRF3\11142001\I869565.raw

7 <110> APPLICANT: Gardella, Thomas J.
 10 Kronenberg, Henry M.
 13 Potts Jr., John T.
 19 <120> TITLE OF INVENTION: PTH Receptor and Screening Assay Utilizing the Same
 25 <130> FILE REFERENCE: 0609.4730000
 29 <140> CURRENT APPLICATION NUMBER: 09/869,565
 C--> 32 <141> CURRENT FILING DATE: 1998-12-31 ✓
 37 <150> PRIOR APPLICATION NUMBER: PCT/US98/27862
 40 <151> PRIOR FILING DATE: 1998-12-31
 46 <160> NUMBER OF SEQ ID NOS: 2
 52 <170> SOFTWARE: PatentIn Ver. 2.0
 58 <210> SEQ ID NO: 1
 61 <211> LENGTH: 1320
 64 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial Sequence
 73 <220> FEATURE:
 76 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA
 82 <220> FEATURE:
 85 <221> NAME/KEY: CDS
 88 <222> LOCATION: (1)..(1308)
 94 <400> SEQUENCE: 1
 97 atg ggg gcc gcc cggtt atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48
 100 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 103 1 5 10 15
 109 cca gtg ctc agc tcc gca tat gct ctg gag gta ttt gac cgc cta ggc 96
 112 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly
 115 20 25 30
 121 atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg 144
 124 Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val
 127 35 40 45
 133 gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac 192
 136 Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn
 139 50 55 60
 145 tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc 240
 148 Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser
 151 65 70 75 80
 157 atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag 288
 160 Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu
 163 85 90 95
 169 gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca 336
 172 Ala Glu Arg Leu Thr Glu Glu Leu His Ile Ile Ala Gln Val Pro
 175 100 105 110
 181 cct ccg ccg gcc gct gcc gca gta ggc tac gct ggc tgc cgc gtg gcg 384
 184 Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala
 187 115 120 125
 193 gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg 432
 196 Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu

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199	130	135	140		
205	gtg gag ggg ctg tac ttg cac agc ctc atc ttc atg gcc ttt ttc tca			480	
208	Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser				
211	145	150	155	160	
217	gag aag aag tac ctg tgg ggc ttc acc atc ttt ggc tgg ggt cta ccg			528	
220	Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro				
223	165	170	175		
229	gct gtc ttc gtg gct gtg tgg gtc ggt gtc aga gca acc ttg gcc aac			576	
232	Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn				
235	180	185	190		
241	act ggg tgc tgg gat ctg agc tcc ggg cac aag aag tgg atc atc cag			624	
244	Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln				
247	195	200	205		
253	gtg ccc atc ctg gca tct gtt gtg ctc aac ttc atc ctt ttt atc aac			672	
256	Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn				
259	210	215	220		
265	atc atc cgg gtg ctt gcc act aag ctt cgg gag acc aat gcg ggc cgg			720	
268	Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg				
271	225	230	235	240	
277	tgt gac acc agg cag cag tac cgg aag ctg ctc agg tcc acg ttg gtg			768	
280	Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val				
283	245	250	255		
289	ctc gtg ccg ctc ttt ggt gtg cac tac acc gtc ttc atg gcc ttg ccg			816	
292	Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro				
295	260	265	270		
301	tac acc gag gtc tca ggg aca ttg tgg cag atc cag atg cat tat gag			864	
304	Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu				
307	275	280	285		
313	atg ctc ttc aac tcc ttc cag gga ttt ttt gtt gcc atc ata tac tgt			912	
316	Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys				
319	290	295	300		
325	ttc tgc aat ggt gag gtg cag gca gag att agg aag tca tgg agc cgc			960	
328	Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg				
331	305	310	315	320	
337	tgg aca ctg gcg ttg gac ttc aag cgc aaa gca cga agt ggg agt agc			1008	
340	Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser				
343	325	330	335		
349	agc tac agc tat ggc cca atg gtg tct cac acg agt gtg acc aat gtg			1056	
352	Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val				
355	340	345	350		
361	ggc ccc cgt gca gga ctc agc ctc ccc ctc agc ccc cgc ctg cct cct			1104	
364	Gly Pro Arg Ala Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro				
367	355	360	365		
373	gcc act acc aat ggc cac tcc cag ctg cct ggc cat gcc aag cca ggg			1152	
376	Ala Thr Thr Asn Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly				
379	370	375	380		
385	gct cca gcc act gag act gaa acc cta cca gtc act atg gcg gtt ccc			1200	
388	Ala Pro Ala Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro				
391	385	390	395	400	

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397 aag gac gat gga ttc ctt aac ggc tcc tgc tca ggc ctg gat gag gag 1248
 400 Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
 403 405 410 415
 409 gcc tcc ggg tct gcg cgg ccg cct cca ttg ttg cag gaa gga tgg gaa 1296
 412 Ala Ser Gly Ser Ala Arg Pro Pro Leu Leu Gln Glu Gly Trp Glu
 415 420 425 430
 421 aca gtc atg tga ctggcacta gg 1320
 424 Thr Val Met
 427 435
 436 <210> SEQ ID NO: 2
 439 <211> LENGTH: 435
 442 <212> TYPE: PRT
 445 <213> ORGANISM: Artificial Sequence
 451 <220> FEATURE:
 454 <223> OTHER INFORMATION: Description of Artificial Sequence: rat protein sequence
 455 that has been mutated in the laboratory, creating a
 456 deletion in the original sequence.
 461 <400> SEQUENCE: 2
 464 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 467 1 5 10 15
 473 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly
 476 20 25 30
 482 Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val
 485 35 40 45
 491 Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn
 494 50 55 60
 500 Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser
 503 65 70 75 80
 509 Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu
 512 85 90 95
 518 Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro
 521 100 105 110
 527 Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala
 530 115 120 125
 536 Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
 539 130 135 140
 545 Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
 548 145 150 155 160
 554 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro
 557 165 170 175
 563 Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn
 566 180 185 190
 572 Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln
 575 195 200 205
 581 Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn
 584 210 215 220
 590 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
 593 225 230 235 240
 599 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val

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602	245	250	255
608	Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro		
611	260	265	270
617	Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu		
620	275	280	285
626	Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys		
629	290	295	300
635	Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg		
638	305	310	315
644	320	325	330
647	Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser		
653	340	345	350
656	Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val		
662	355	360	365
665	Gly Pro Arg Ala Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro		
671	370	375	380
674	Ala Thr Thr Asn Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly		
680	385	390	395
683	400	405	410
689	Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu		
692	415	420	425
698	Ala Ser Gly Ser Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu		
701	430	435	
707	Thr Val Met		
710			

VERIFICATION SUMMARY

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L:32 M:271 C: Current Filing Date differs, Replaced Current Filing Date